:: GETTING STARTED
-> Wizard

:: QUERY
Expression
-> Quick Query
-> Standard Query
-> Batch Query
-> BLAST
-> Probe Match
-> UCSC Query
Genotyping
-> Quick Query
-> Standard Query
-> Batch Query
-> UCSC Query
-> SNP Finder

:: CURRENT QUERY
1 probe sets
-> Annotations
-> Show Orthologs
-> GO Browser
-> Export

:: QUERY HISTORY
Annotation Views
-> Expression
-> Genotyping
-> BLAST Status
-> New Folder
-> Expression Queries
-> (1)All Descriptions (M12625_at)
-> (1)All Descriptions (U23752_at)
-> (1)All Descriptions (HG1800-HT1823_at)
-> (1)All Descriptions (U15008_at)
-> (1)All Descriptions (HG3523)
-> Genotyping Queries

Full Record

Details for HUGENEFL:M12625_AT

Full Screen

NetAffx Links	Cluster Members Consensus/Exemplar

GeneChip Array Information

Probe Set ID	M12625_at
GeneChip Array	HumanGeneFL Array
Organism Common Name	Human

Probe Design Information

Transcript ID	M12625
Sequence Type	Exemplar sequence
Representative Public ID	M12625 NCBI
Target Description	M12625, class B, 20 probes, 13 in M12625mRNA 893-1259: 7 in reverseSequence, 1599-1683, Human lecithin-cholesterol acyltransferase mRNA, complete cds, with 5' and 3' flanking DNA sequences

Genomic Alignment of Target Sequence

Assembly	April 2003 (NCBI 33)		
Alignment(s)	**Position**	**% Identity**	**Cytoband**
	chr16: 67749925-67750484 (-) UCSC	100	q22.1

Overlapping Transcripts	**Representative Transcript**	**UniGene Description**	**Position**
	M12625 NCBI	lecithin-cholesterol acyltransferase	chr16:67749888-67754507 (-) UCSC

Public Domain and Genome References

Gene Title	lecithin-cholesterol acyltransferase
Gene Symbol	LCAT HGNC
Chromosomal Location	16q22.1
UniGene ID	Hs.387239 NCBI (FULL LENGTH)
Ensembl	ENSG00000103080 Ensembl
LocusLink	3931 NCBI
SwissProt	AAP88750 EMBL-EBI P04180 EMBL-EBI
EC	2.3.1.43
OMIM	606967 NCBI

RefSeq Protein ID NP_000220 NCBI

RefSeq

RefSeq Transcript ID	RefSeq Title
NM_000229 NCBI	lecithin-cholesterol acyltransferase precursor

Functional Annotations

Ortholog

ID	Title	Organism	Type
MG-U74AV2:103023_AT	lecithin cholesterol acyltransferase	Mouse	Curated Ortholog
MG-U74AV2:161759_R_AT	lecithin cholesterol acyltransferase	Mouse	Curated Ortholog
MOE430A:1417043_AT	lecithin cholesterol acyltransferase	Mouse	Curated Ortholog
MU11KSUBA:J05154_S_AT	lecithin cholesterol acyltransferase	Mouse	Curated Ortholog
RAE230A:1367887_AT	lecithin cholesterol acyltransferase	Rat	Curated Ortholog
RG-U34A:X54096_AT	lecithin cholesterol acyltransferase	Rat	Curated Ortholog
MOUSE430_2:1417043_AT	lecithin cholesterol acyltransferase	Mouse	Curated Ortholog
MOUSE430A_2:1417043_AT	lecithin cholesterol acyltransferase	Mouse	Curated Ortholog

Gene Ontology

GO Biological Process (view graph)

ID	Description	Evidence	Links
6629	lipid metabolism	inferred from electronic annotation	QuickGO AmiGO

GO Cellular Component (view graph)

ID	Description	Evidence	Links
5576	extracellular	not recorded	QuickGO AmiGO

GO Molecular Function (view graph)

ID	Description	Evidence	Links
4607	phosphatidylcholine-sterol O-acyltransferase activity	inferred from electronic annotation	QuickGO AmiGO
8415	acyltransferase activity	inferred from electronic annotation	QuickGO AmiGO
16740	transferase activity	inferred from electronic annotation	QuickGO AmiGO

Protein Similarities

Method	ID	Description	E-Value
blast	32879837		0.0
blast	4557892	lecithin-cholesterol acyltransferase precursor [Homo sapiens]	0.0

Protein Families

Method	ID	Description	E-Value
ec	LCAT_HUMAN	LCAT_HUMAN EC:2.3.1.43:PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43) (LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE).	1.85E-171

Database	ID	Description	E-Value

Protein Domains

scop	d1tca__	d1tca__ SCOP:c.69.1.17:| Triacylglycerol lipase	5.3E-8
pfam	LACT	Lecithin:cholesterol acyltransferase	1.7E-182
InterPro	IPR003386 EMBL-EBI	Lecithin:cholesterol acyltransferase	
InterPro	IPR008262 EMBL-EBI	Lipase, active site	

Trans Membrane

ID	Number Of Domains	Probability of Interior N-Terminus
NP_000220	2	0.05945

Target Sequence

Sequence

>HUGENEFL:M12625_AT

ctttcaactacacaggccgtgacttccaacgcttctttgcagacctgcactttgaggaagg
ctggtacatgtggctgcagtcacgtgacctcctggcaggactcccagcacctggtgtgga
agtatactgtctttacggcgtgggcctgcccacgccccgcacctacatctacgaccacgg
cttcccctacacggaccctgtgggtgtgctctatgaggatggtgatgacacggtggcgac
ccgcagcaccgagctctgtggcctgtggcagggccgccagccacagcctgtgcacctgct
gcccctgcacgggatacagcatctcaacatggtcttcagcaacctgaccctggagcacat
caatgccatcctgctgggtgcctaccgccagggtccccctgcatccccgactgccagccc
agagcccccgcctcctgaataaagaccttcctttgctaccgtaagccctgatggctatgt
ttcaggttgaagggaggcactagagtcccacactaggtttcactcctcaccagccacagg
ctcagtgctgtgtgcagtg

Probe Info

Probe Sequence(5'-3')	Probe X	Probe Y	Probe Interrogation Position	Strandedness
CTTCAACTACACAGGCCGTGACTTC	152	127	1161	Antisense
CTACACAGGCCGTGACTTCCAACGC	153	127	1167	Antisense
CCAACGCTTCTTTGCAGACCTGCAC	154	127	1185	Antisense
CCTGCACTTTGAGGAAGGCTGGTAC	155	127	1203	Antisense
CATGTGGCTGCAGTCACGTGACCTC	156	127	1227	Antisense
GCTGCAGTCACGTGACCTCCTGGCA	157	127	1233	Antisense
CCTGGCAGGACTCCCAGCACCTGGT	158	127	1251	Antisense
GGACCCTGTGGGTGTGCTCTATGAG	159	127	1353	Antisense
TGTGCTCTATGAGGATGGTGATGAC	160	127	1365	Antisense
GGCGACCCGCAGCACCGAGCTCTGT	161	127	1395	Antisense
CCTGACCCTGGAGCACATCAATGCC	162	127	1503	Antisense
GCACATCAATGCCATCCTGCTGGGT	163	127	1515	Antisense
CATCCTGCTGGGTGCCTACCGCCAG	164	127	1527	Antisense
CTTTGCTACCGTAAGCCCTGATGGC	165	127	1611	Antisense
TACCGTAAGCCCTGATGGCTATGTT	166	127	1617	Antisense
AAGCCCTGATGGCTATGTTTCAGGT	167	127	1623	Antisense
CTATGTTTCAGGTTGAAGGGAGGCA	168	127	1635	Antisense
GGAGGCACTAGAGTCCCACACTAGG	169	127	1653	Antisense
GTCCCACACTAGGTTTCACTCCTCA	170	127	1665	Antisense
CACAGGCTCAGTGCTGTGTGCAGTG	171	127	1695	Antisense